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1

SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> Novel genes of Candida albicans and the proteins  
coded by these genes.

<130> 2517 PCT SEQUENCES IN FRENCH

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<150> FR 9907250

<151> 1999-06-09

<160> 32

<170> PatentIn Ver. 2.1

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<211> 747

<212> DNA

<213> Candida albicans

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<221> CDS

<222> (1)..(747)

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<221> modified\_base

<222> (136)..(138)

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cta act ata aat gat gta tca aaa tca gga ttt gga tac aat ccg tcc 96  
 Leu Thr Ile Asn Asp Val Ser Lys Ser Gly Phe Gly Tyr Asn Pro Ser  
           20                 25                 30

ata gga cca ata tca aat act att acc cta gaa tct tca ctg gta tta 144  
 Ile Gly Pro Ile Ser Asn Thr Ile Thr Leu Glu Ser Ser Ser Val Leu  
           35                 40                 45

tta aat aaa cgt aca ata tca tta aca cca aca tca tct gac tcc att 192  
 Leu Asn Lys Arg Thr Ile Ser Leu Thr Pro Thr Ser Ser Asp Ser Ile  
           50                 55                 60

tat gat aga aat att atc acg aaa aag cca cac gaa atc aac tta tct 240  
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       65                 70                 75                 80

tcg tta tca ttt ttg ttt tgt gag att att agt tgg gca cac tct aat 288  
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       85                 90                 95

tcc aaa ggc att caa gat tta gaa aat cgt tta aac gga tta ggt tat 336  
 Ser Lys Gly Ile Gln Asp Leu Glu Asn Arg Leu Asn Gly Leu Gly Tyr  
       100                105                110

caa ata ggt caa cga tat ctc gaa ttg tgt aaa ata aga gaa ggt ttt 384  
 Gln Ile Gly Gln Arg Tyr Leu Glu Leu Cys Lys Ile Arg Glu Gly Phe  
       115                120                125

aaa aac agt aaa cga gag att aga ctt ttg gaa atg tta caa ttt att 432  
 Lys Asn Ser Lys Arg Glu Ile Arg Leu Leu Glu Met Leu Gln Phe Ile  
       130                135                140

cat ggt ccg ttc tgg aaa ttg att ttt ggt aaa act gct aat gaa tta 480  
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       145                150                155                160

gaa aaa tcg caa gat ttg ccc aat gaa tat atg att gtg gag aat gtg 528  
 Glu Lys Ser Gln Asp Leu Pro Asn Glu Tyr Met Ile Val Glu Asn Val  
 165 170 175

cca tta tta aat aga ttt att agt ata cct aag gag tat ggc gac tta 576  
 Pro Leu Leu Asn Arg Phe Ile Ser Ile Pro Lys Glu Tyr Gly Asp Leu  
 180 185 190

aat tgt tca gca ttt gtt gcg ggt ata att gag gga gca ctt gat aat 624  
 Asn Cys Ser Ala Phe Val Ala Gly Ile Ile Glu Gly Ala Leu Asp Asn  
 195 200 205

agt gga ttc aat gcc gat gtt aca gca cac acg gtc gct aca gat gca 672  
 Ser Gly Phe Asn Ala Asp Val Thr Ala His Thr Val Ala Thr Asp Ala  
 210 215 220

aat cca tta aga aca gta ttt ttg atc aag ttt gac gat tct gtt tta 720  
 Asn Pro Leu Arg Thr Val Phe Leu Ile Lys Phe Asp Asp Ser Val Leu  
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Ile Gly Pro Ile Ser Asn Thr Ile Thr Leu Glu Ser Ser Ser Val Leu  
35 40 45

Leu Asn Lys Arg Thr Ile Ser Leu Thr Pro Thr Ser Ser Asp Ser Ile  
50 55 60

Tyr Asp Arg Asn Ile Ile Thr Lys Lys Pro His Glu Ile Asn Leu Ser  
65 70 75 80

Ser Leu Ser Phe Leu Phe Cys Glu Ile Ile Ser Trp Ala His Ser Asn  
85 90 95

Ser Lys Gly Ile Gln Asp Leu Glu Asn Arg Leu Asn Gly Leu Gly Tyr  
100 105 110

Gln Ile Gly Gln Arg Tyr Leu Glu Leu Cys Lys Ile Arg Glu Gly Phe  
115 120 125

Lys Asn Ser Lys Arg Glu Ile Arg Leu Leu Glu Met Leu Gln Phe Ile  
130 135 140

His Gly Pro Phe Trp Lys Leu Ile Phe Gly Lys Thr Ala Asn Glu Leu  
145 150 155 160

Glu Lys Ser Gln Asp Leu Pro Asn Glu Tyr Met Ile Val Glu Asn Val  
165 170 175

Pro Leu Leu Asn Arg Phe Ile Ser Ile Pro Lys Glu Tyr Gly Asp Leu  
180 185 190

Asn Cys Ser Ala Phe Val Ala Gly Ile Ile Glu Gly Ala Leu Asp Asn  
195 200 205

Ser Gly Phe Asn Ala Asp Val Thr Ala His Thr Val Ala Thr Asp Ala  
210 215 220

Asn Pro Leu Arg Thr Val Phe Leu Ile Lys Phe Asp Asp Ser Val Leu  
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Glu Lys Ile Ser Ser Lys Thr Ser Ser Ile Asn Leu Tyr Gln Asp Leu  
20 25 30

cta aga gct atg atc aac gaa cgt atg gct ccg gaa tta ttg cca tac 144  
Leu Arg Ala Met Ile Asn Glu Arg Met Ala Pro Glu Leu Leu Pro Tyr  
35 40 45

aaa caa gat tta atg tcc act gtt tta aca atg atg tct aac caa caa 192  
Lys Gln Asp Leu Met Ser Thr Val Leu Thr Met Met Ser Asn Gln Gln  
50 55 60

caa tat tta tta gaa tct cac gaa tat ggt gat atg aat ggc gac agt 240  
Gln Tyr Leu Leu Glu Ser His Glu Tyr Gly Asp Met Asn Gly Asp Ser  
65 70 75 80

ggt gta tta tcc gga gac ttt aaa tta caa cta atg att atc gaa act	288		
Gly Val Leu Ser Gly Asp Phe Lys Leu Gln Leu Met Ile Ile Glu Thr			
85	90	95	
gat tta gag cgt ctc aac tat att gtt cga tta tac ata cga act cga	336		
Asp Leu Glu Arg Leu Asn Tyr Ile Val Arg Leu Tyr Ile Arg Thr Arg			
100	105	110	
ttg agt aag ttg aat aaa ttt act att ttt tac atc aat gaa agc agt	384		
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115	120	125	
caa aat gat aat tta ttg tcc aaa gag gaa aga gat tat ata cac aaa	432		
Gln Asn Asp Asn Leu Leu Ser Lys Glu Glu Arg Asp Tyr Ile His Lys			
130	135	140	
tat ttc cag att ttg actcaa tta tat aac aac tgt ttc ctc aaa aaa	480		
Tyr Phe Gln Ile Leu Thr Gln Leu Tyr Asn Asn Cys Phe Leu Lys Lys			
145	150	155	160
cta cca caa atg ttg acc tat ttg gat gac acc agt ggt gga caa tca	528		
Leu Pro Gln Met Leu Thr Tyr Leu Asp Asp Thr Ser Gly Gly Gln Ser			
165	170	175	
atg atc gtt gag cca gat tta gac cag cct gtg ttt atc aaa tgt acc	576		
Met Ile Val Glu Pro Asp Leu Asp Gln Pro Val Phe Ile Lys Cys Thr			
180	185	190	
ctg gaa gtc cca ata tta cta gat tac gac ggt gct aca gag ata gat	624		
Ser Glu Val Pro Ile Leu Leu Asp Tyr Asp Gly Ala Thr Glu Ile Asp			
195	200	205	
tta gaa tta ata aaa aag gga gtc tac gtg gtg aaa tac agc cta gtc	672		
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Leu Arg Ala Met Ile Asn Glu Arg Met Ala Pro Glu Leu Leu Pro Tyr  
35 40 45

Lys Gln Asp Leu Met Ser Thr Val Leu Thr Met Met Ser Asn Gln Gln  
50 55 60

Gln Tyr Leu Leu Glu Ser His Glu Tyr Gly Asp Met Asn Gly Asp Ser  
 65                      70                      75                      80

Gly Val Leu Ser Gly Asp Phe Lys Leu Gln Leu Met Ile Ile Glu Thr  
                   85                   90                   95

Asp Leu Glu Arg Leu Asn Tyr Ile Val Arg Leu Tyr Ile Arg Thr Arg  
100 105 110

Leu Ser Lys Leu Asn Lys Phe Thr Ile Phe Tyr Ile Asn Glu Ser Ser  
 115                    120                    125

Gln Asn Asp Asn Leu Leu Ser Lys Glu Glu Arg Asp Tyr Ile His Lys  
 130                    135                    140

Tyr Phe Gln Ile Leu Thr Gln Leu Tyr Asn Asn Cys Phe Leu Lys Lys  
 145 150 155 160

Leu Pro Gln Met Leu Thr Tyr Leu Asp Asp Thr Ser Gly Gly Gln Ser  
 165 170 175

Met Ile Val Glu Pro Asp Leu Asp Gln Pro Val Phe Ile Lys Cys Thr  
 180 185 190

Ser Glu Val Pro Ile Leu Leu Asp Tyr Asp Gly Ala Thr Glu Ile Asp  
 195 200 205

Leu Glu Leu Ile Lys Lys Gly Val Tyr Val Val Lys Tyr Ser Leu Val  
 210 215 220

Lys Arg Tyr Ile Asp Ile Gly Asp Val Val Leu Ile  
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tta aaa gaa aag aaa gtc tca aga tgg agg caa aag caa cag gaa	144		
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50	55	60	
aaa att cac caa gaa aat atc gag aag atg gct caa atg tca gag gaa	240		
Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu			
65	70	75	80
gag att ttg caa gag cgt gag gag tta cta aag ggt tta gat cct aaa	288		
Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys			
85	90	95	
tta att gaa agt ttg att ggt aga tcc aag aaa agg gaa gca aca gac	336		
Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp			
100	105	110	
cat gaa cac aat gga cat gct cat gaa cat gca gag gga tac cat gga	384		
His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly			
115	120	125	
tgg att gga tca atg aaa act tct gaa gga tta aca gat tta tct caa	432		
Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln			
130	135	140	
tta gat aag gaa gat gtg gac cgt gca ttg ggt ata agt tca tta tcc	480		
Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser			
145	150	155	160
tta tct gaa cct gag ggt ggc agt aat acg aaa aaa gtc gct ttc gac	528		
Leu Ser Glu Pro Glu Gly Gly Ser Asn Thr Lys Lys Val Ala Phe Asp			
165	170	175	

gat aat atc aag acg gtt aaa ttt gaa gat ttg gat gat gga att gaa 576  
Asp Asn Ile Lys Thr Val Lys Phe Glu Asp Leu Asp Asp Gly Ile Glu  
180 185 190

ttg gat cca aat gga tgg gag gac gtt act gat gtc aat gaa tta gtt 624  
Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val  
195 200 205

cct aat aat gat cac att gca cct gac gat tac cag att aat cct gat 672  
Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp  
210 215 220

agc gat gaa gaa gga ttg aat aat act gtt cat ttt aca aaa ccc aaa 720  
Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys  
225 230 235 240

cag cca gat ttg gat ata aat gat ccc gat ttc ttt gat aag cta cat 768  
Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His  
245 250 255

gag aaa tac tat cct gat ttg cct aaa gaa aca gaa aag ttg tca tgg 816  
Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp  
260 265 270

atg aca cag cca atg cca aaa caa ttg tct acc gtt tat gaa tca ata 864  
Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile  
275 280 285

tct gat atg aga ttt gac ttt aaa gga gat tta att gaa ttg ggt cca 912  
Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Gly Pro  
290 295 300

gag gga gaa gaa cca aaa gat agt tca tcc gaa ata cct act tat atg 960  
Glu Gly Glu Glu Pro Lys Asp Ser Ser Ser Glu Ile Pro Thr Tyr Met  
305 310 315 320

gga ctt cat cat cat tcg gag aac cca cat atg gca ggt tat aca ttg 1008  
 Gly Leu His His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu  
 325 330 335

ggt gag ttg gca cat tta gcc aga tcg act tta gct gga caa aga tgc 1056  
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 340 345 350

ttg agc att caa aca tta ggg aga atc tta cat aaa ttg gga tta cat 1104  
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 355 360 365

aaa tac agt ata cta cca aaa aca gac tca gat gat cag agt ttt aca 1152  
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 370 375 380

gat gaa atc aaa caa cta tca ctt gac ttt gaa gat atg atg tgg gac 1200  
 Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp  
 385 390 395 400

ttg ata gac caa tta cga atc att gaa aca ata aca gag gca gct gat 1248  
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 405 410 415

gaa aaa aag acc aga aac tta tct gtc aga aat tat gca ata gag gca 1296  
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 420 425 430

ttg tgg tta tat aga act gga ggt gga aga cca gag ata act aaa caa 1344  
 Leu Trp Leu Tyr Arg Thr Gly Gly Arg Pro Glu Ile Thr Lys Gln  
 435 440 445

acc gaa gag gat ttg ata gca caa gca gtt cag aaa taa 1383  
 Thr Glu Glu Asp Leu Ile Ala Gln Ala Val Gln Lys  
 450 455 460

&lt;211&gt; 461

&lt;212&gt;

&lt;213&gt; Candida albicans

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20 25 30

Leu Lys Glu Lys Lys Val Ser Arg Trp Arg Gln Lys Gln Gln Gln  
35 40 45

Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser  
50 55 60

Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu  
65 70 75 80

Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys  
85 90 95

Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp  
100 105 110

His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly  
115 120 125

Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln  
130 135 140

Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser  
145 150 155 160

Leu Ser Glu Pro Glu Gly Ser Asn Thr Lys Lys Val Ala Phe Asp  
165 170 175

Asp Asn Ile Lys Thr Val Lys Phe Glu Asp Leu Asp Asp Gly Ile Glu  
180 185 190

Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val  
195 200 205

Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp  
210 215 220

Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys  
225 230 235 240

Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His  
245 250 255

Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp  
260 265 270

Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile  
275 280 285

Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Gly Pro  
290 295 300

Glu Gly Glu Glu Pro Lys Asp Ser Ser Ser Glu Ile Pro Thr Tyr Met  
305 310 315 320

Gly Leu His His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu  
325 330 335

Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys  
340 345 350

Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His  
355 360 365

Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr  
370 375 380

Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp  
385 390 395 400

Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp  
405 410 415

Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala  
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 35 40 45

cag agc aca act tcc cca aaa act act gaa atc cgt tca gag gct tcc 192  
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 50 55 60

aaa att cac caa gaa aat atc gag aag atg gct caa atg tca gag gaa 240  
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 65 70 75 80

gag att ttg caa gag cgt gag gag tta cta aag ggt tta gac cct aaa 288  
 Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys  
 85 90 95

tta att gaa agt ttg att ggt aga tcc aag aaa agg gaa gca aca gac 336  
 Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp  
 100 105 110

cat gaa cac aat gga cat gct cat gaa cat gca gag gga tac cat gga 384  
 His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly  
 115 120 125

tgg att gga tca atg aaa act tct gaa gga tta aca gat tta tct caa 432  
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 130 135 140

tta gat aag gaa gat gtg gac cgt gct ttg ggt ata agt tca tta tcc 480  
 Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser  
 145 150 155 160

tta tct gaa cct gag ggt ggc agc aat acg aaa aaa gtc gct ttc gac 528  
 Leu Ser Glu Pro Glu Gly Gly Ser Asn Thr Lys Lys Val Ala Phe Asp  
 165 170 175

gat aat atc aag acg gtt aaa ttt gaa gct ttg gat gat gaa att gaa 576  
 Asp Asn Ile Lys Thr Val Lys Phe Glu Ala Leu Asp Asp Glu Ile Glu  
 180 185 190

ttg gat cca aat gga tgg gag gac gtt act gat gtc aat gaa tta gtt 624  
 Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val  
 195 200 205

cct aat aat gat cac att gca cct gac gat tac cag att aat cct gat 672  
 Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp  
 210 215 220

agc gat gaa gaa gga ttg aat aat act gtt cat ttt aca aaa ccc aaa 720  
 Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys  
 225 230 235 240

cag cca gat ttg gat ata aat gat ccc gat ttc ttt gat aag cta cat 768  
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 245 250 255

gag aaa tac tat cct gat ttg cct aaa gaa aca gaa aag ttg tca tgg 816  
 Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp  
 260 265 270

atg aca cag cca atg cca aaa caa ttg tct aca gtt tat gaa tca ata 864  
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 275 280 285

tct gat atg aga ttt gac ttc aaa gga gat tta att gaa ttg agc gca 912  
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 Glu Gly Glu Glu Pro Lys Asp Ser Ser Phe Glu Ile Pro Thr Tyr Met  
 305 310 315 320

gga ctt cat cat cat tcg gag aac cca cat atg gca ggt tat aca ttg 1008  
 Gly Leu His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu  
 325 330 335

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 340 345 350

ttg agc att caa aca tta ggg aga ata tta cat aaa ttg gga tta cat 1104  
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 355 360 365

aaa tac agt ata cta cca aaa aca gac tca gat gat cag agt ttt aca 1152  
 Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr  
 370 375 380

gat gaa atc aaa caa cta tca ctt gac ttt gaa gat atg atg tgg gac 1200  
 Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp  
 385 390 395 400

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 405 410 415

gaa aaa aag acc aga aac tta tct gtc aga aat tat gca ata gag gca 1296  
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 420 425 430

ttg tgg tta tat aga act gga ggt gga aga cca gag ata act aaa caa 1344  
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<212>

<213> Candida albicans

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35 40 45

Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser  
50 55 60

Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu  
65 70 75 80

Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys  
85 90 95

Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp  
100 105 110

His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly  
115 120 125

Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln  
130 135 140

Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser  
145 150 155 160

Leu Ser Glu Pro Glu Gly Gly Ser Asn Thr Lys Lys Val Ala Phe Asp  
165 170 175

Asp Asn Ile Lys Thr Val Lys Phe Glu Ala Leu Asp Asp Glu Ile Glu  
180 185 190

Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val  
195 200 205

Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp  
210 215 220

Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys  
225 230 235 240

Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His  
245 250 255

Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp  
260 265 270

Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile  
275 280 285

Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Ser Ala  
290 295 300

Glu Gly Glu Glu Pro Lys Asp Ser Ser Phe Glu Ile Pro Thr Tyr Met  
305 310 315 320

Gly Leu His His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu  
325 330 335

Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys  
340 345 350

Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His  
355 360 365

Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr  
370 375 380

Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp  
385 390 395 400

Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp  
 405 410 415

Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala  
 420 425 430

Leu Trp Leu Tyr Arg Thr Gly Gly Arg Pro Glu Ile Thr Lys Gln  
 435 440 445

Thr Glu Glu Asp Leu Ile Ala Gln Ala Val Gln Lys  
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<210> 9

<211> 2262

<212> DNA

<213> Candida albicans

<220>

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<222> (1) .. (2262)

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<222> (1828) .. (1830)

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 Met Ala Ala Ala Pro Pro Pro Ala Lys Asn Gln Gly Lys Ala Lys  
 1 5 10 15

cag cat gtt aca ggt gcc agg ttc cgt cag cga aaa atc tcg gta aag 95  
 Gln His Val Thr Gly Ala Arg Phe Arg Gln Arg Lys Ile Ser Val Lys

20 25 30

cag	ccc	tta	act	att	tat	aaa	cag	aga	gac	cta	cct	act	cta	gat	agc	144
Gln	Pro	Leu	Thr	Ile	Tyr	Lys	Gln	Arg	Asp	Leu	Pro	Thr	Leu	Asp	Ser	
35							40							45		
aat	gag	tta	gag	cct	agt	caa	gtc	cat	cat	tta	aat	tct	aat	gcg	tca	192
Asn	Glu	Leu	Glu	Pro	Ser	Gln	Val	His	His	Leu	Asn	Ser	Asn	Ala	Ser	
50							55							60		
tca	tca	tca	aca	caa	caa	ccg	aga	gac	ctt	cat	gca	gtt	gaa	act	ggg	240
Ser	Ser	Ser	Thr	Gln	Gln	Pro	Arg	Asp	Leu	His	Ala	Val	Glu	Thr	Gly	
65							70							75		80
gtt	gac	aag	aat	gag	gaa	gag	gaa	gtg	cat	ctt	cag	caa	gtt	atc	aat	288
Val	Asp	Lys	Asn	Glu	Glu	Glu	Glu	Val	His	Leu	Gln	Gln	Val	Ile	Asn	
85							90							95		
gct	gca	caa	aaa	gca	ctt	ttg	ggt	tcg	aaa	aaa	gaa	gaa	aaa	agc	agt	336
Ala	Ala	Gln	Lys	Ala	Leu	Leu	Gly	Ser	Lys	Lys	Glu	Glu	Lys	Ser	Ser	
100							105							110		
gat	atg	tat	att	ccc	aca	ccg	gac	gct	tcg	agg	ata	tgg	ccc	gag	gca	384
Asp	Met	Tyr	Ile	Pro	Thr	Pro	Asp	Ala	Ser	Arg	Ile	Trp	Pro	Glu	Ala	
115							120							125		
cac	aag	tat	tac	aag	gat	caa	aag	ttc	aag	cag	cca	gag	aca	tat	atc	432
His	Lys	Tyr	Tyr	Lys	Asp	Gln	Lys	Phe	Lys	Gln	Pro	Glu	Thr	Tyr	Ile	
130							135							140		
aag	ttt	agt	gcg	aca	gta	gag	gac	aca	gtg	ggt	gtg	gag	tac	aat	atg	480
Lys	Phe	Ser	Ala	Thr	Val	Glu	Asp	Thr	Val	Gly	Val	Glu	Tyr	Asn	Met	
145							150							155		160
gac	gag	gta	gat	gaa	aag	ttt	tat	aga	gag	aca	cta	tgc	aag	tac	tat	528
Asp	Glu	Val	Asp	Glu	Lys	Phe	Tyr	Arg	Glu	Thr	Leu	Cys	Lys	Tyr	Tyr	
165							170							175		

ccc aaa aag aaa aac aag tca gat gag aac aat cga aag tgt act gaa 576  
 Pro Lys Lys Lys Asn Lys Ser Asp Glu Asn Asn Arg Lys Cys Thr Glu  
 180 185 190

ttg gag ttt gaa aca atc tgt gac aag ttg gaa aag acc att gaa gca 624  
 Leu Glu Phe Glu Thr Ile Cys Asp Lys Leu Glu Lys Thr Ile Glu Ala  
 195 200 205

cga caa ccg ttt ttg tct atg gac ccc agc aac att cta tcg tac gag 672  
 Arg Gln Pro Phe Leu Ser Met Asp Pro Ser Asn Ile Leu Ser Tyr Glu  
 210 215 220

gag ttg tcg tcg tac att gtg gat cag ttt aaa agt gca gtg aaa aca 720  
 Glu Leu Ser Ser Tyr Ile Val Asp Gln Phe Lys Ser Ala Val Lys Thr  
 225 230 235 240

agc aac ccg tat att gtt acc aat ggt ggg aat cta gag tat ata tcg 768  
 Ser Asn Pro Tyr Ile Val Thr Asn Gly Gly Asn Leu Glu Tyr Ile Ser  
 245 250 255

acg aca gct tta aaa gag aga ttg tcg aag gaa ata aag tat gaa ccg 816  
 Thr Thr Ala Leu Lys Glu Arg Leu Ser Lys Glu Ile Lys Tyr Glu Pro  
 260 265 270

ttt gtt act att ttt gat aag aac caa atg tcc aca agt gcg gtg aga 864  
 Phe Val Thr Ile Phe Asp Lys Asn Gln Met Ser Thr Ser Ala Val Arg  
 275 280 285

cct att ccc aaa ttg ttt gag ttg ttc ggc aga cct gtt tat gat cat 912  
 Pro Ile Pro Lys Leu Phe Glu Leu Phe Gly Arg Pro Val Tyr Asp His  
 290 295 300

tgg aag gag aga aaa ata gaa aga aag ggc aaa acc atc cag ccc aca 960  
 Trp Lys Glu Arg Lys Ile Glu Arg Lys Gly Lys Thr Ile Gln Pro Thr  
 305 310 315 320

ctc aaa ttt gag gat cct aac tcg aac gaa aag gaa aac gac aat gac 1008  
 Leu Lys Phe Glu Asp Pro Asn Ser Asn Glu Lys Glu Asn Asp Asn Asp  
 325 330 335

cca tat ata tgt ttc aga cga cgt gag ttt agg caa gca aga aag acg 1056  
 Pro Tyr Ile Cys Phe Arg Arg Arg Glu Phe Arg Gln Ala Arg Lys Thr  
 340 345 350

aga aga gcc gat aca att ggt gca gag aga ata aga ctg atg caa aag 1104  
 Arg Arg Ala Asp Thr Ile Gly Ala Glu Arg Ile Arg Ser Met Gln Lys  
 355 360 365

tcg ttg cac cgc gca cgt gat ttg ata atg agt gtt agt gaa aga gag 1152  
 Ser Leu His Arg Ala Arg Asp Leu Ile Met Ser Val Ser Glu Arg Glu  
 370 375 380

atc ctc aaa ctc gac aat ttt caa gca gag cat gaa ttg ttt aaa gcc 1200  
 Ile Leu Lys Leu Asp Asn Phe Gln Ala Glu His Glu Leu Phe Lys Ala  
 385 390 395 400

agg tgc gct acc aag gct tgt aag agg gag ctc aat atc aag ggt gac 1248  
 Arg Cys Ala Thr Lys Ala Cys Lys Arg Glu Leu Asn Ile Lys Gly Asp  
 405 410 415

gaa tac ttg ttc ttt ccg cat aaa aag aag aaa att gtt cgt act gaa 1296  
 Glu Tyr Leu Phe Phe Pro His Lys Lys Lys Ile Val Arg Thr Glu  
 420 425 430

gat gaa gaa agg gag aag aag aga gaa aag aag aag caa gac caa gaa 1344  
 Asp Glu Glu Arg Glu Lys Lys Arg Glu Lys Lys Gln Asp Gln Glu  
 435 440 445

ctt gca ctc aag caa caa gca cta cag caa cag cag caa caa cca 1392  
 Leu Ala Leu Lys Gln Gln Gln Ala Leu Gln Gln Gln Gln Gln Pro  
 450 455 460

cca caa cca cca caa gca cca tca aaa caa gat ggt aca tca acg 1440  
 Pro Gln Pro Pro Gln Gln Ala Pro Ser Lys Gln Asp Gly Thr Ser Thr  
 465 470 475 480

agc cag cct tat gtc aaa ctc cca ccc gca aaa gtt cca gat atg gat 1488  
 Ser Gln Pro Tyr Val Lys Leu Pro Pro Ala Lys Val Pro Asp Met Asp  
 485 490 495

ctt gtt aca gtt tcg ttg gta tta aag gaa aag aac gaa acc atc aaa 1536  
 Leu Val Thr Val Ser Leu Val Leu Lys Glu Lys Asn Glu Thr Ile Lys  
 500 505 510

cgt gct gtg ttg gag aaa ttg cgc aag aga aag gaa cac gac aag gga 1584  
 Arg Ala Val Leu Glu Lys Leu Arg Lys Arg Lys Glu His Asp Lys Gly  
 515 520 525

ttt atc aat ttg aca gac gat ccg tat cag cca ttt ttc gat att tca 1632  
 Phe Ile Asn Leu Thr Asp Asp Pro Tyr Gln Pro Phe Phe Asp Ile Ser  
 530 535 540

acc aat agg gcc gaa gag ttg agc cat att ccg tat tcg tcg att gcg 1680  
 Thr Asn Arg Ala Glu Glu Leu Ser His Ile Pro Tyr Ser Ser Ile Ala  
 545 550 555 560

gcc aca cac tat cac caa ttc aac aca tcg aac tac atg aac gac caa 1728  
 Ala Thr His Tyr His Gln Phe Asn Thr Ser Asn Tyr Met Asn Asp Gln  
 565 570 575

ctt aaa aag cta ctt gaa gag aaa aaa cct tta cct ggt gta aaa acg 1776  
 Leu Lys Lys Leu Leu Glu Glu Lys Lys Pro Leu Pro Gly Val Lys Thr  
 580 585 590

ttt ttg ggt tct aac ggg gag ttg gta cca tcg aag gca ttt cca cat 1824  
 Phe Leu Gly Ser Asn Gly Glu Leu Val Pro Ser Lys Ala Phe Pro His  
 595 600 605

ttg ctg tcg ttg ctt gag gaa aag tat aag gcg aca agt ggg tat att 1872  
 Leu Ser Ser Leu Leu Glu Glu Lys Tyr Lys Ala Thr Ser Gly Tyr Ile  
 610 615 620

gaa cga tta ttg caa agc gtg gag acg caa gat ttt agt tca tac acc 1920  
 Glu Arg Leu Leu Gln Ser Val Glu Thr Gln Asp Phe Ser Ser Tyr Thr  
 625 630 635 640

aat ggc ttt aaa gat gtt gag cca aaa gaa aca aat gaa cct gtt atg 1963  
 Asn Gly Phe Lys Asp Val Glu Pro Lys Glu Thr Asn Glu Pro Val Met  
 645 650 655

gcg ttt ccc cag aga ata cgt cga aga gtg ggc agg gct ggc agg gtt 2016  
 Ala Phe Pro Gln Arg Ile Arg Arg Val Gly Arg Ala Gly Arg Val  
 660 665 670

ttt ttg gac cac cag caa gag tac ccg caa ccg aat ttt cag caa gac 2064  
 Phe Leu Asp His Gln Gln Glu Tyr Pro Gln Pro Asn Phe Gln Gin Asp  
 675 680 685

aca gat cgt gtg gga ggt atc cca gat gtg tat tgt aaa gag gat gcc 2112  
 Thr Asp Arg Val Gly Gly Ile Pro Asp Val Tyr Cys Lys Glu Asp Ala  
 690 695 700

att aaa cga tta cag tca aag tgg aag ttc gat aca gaa tat aaa aca 2160  
 Ile Lys Arg Leu Gln Ser Lys Trp Lys Phe Asp Thr Glu Tyr Lys Thr  
 705 710 715 720

act gaa cca ttt agt ttg gat cct tca aag ttg aat ggt att agt cca 2208  
 Thr Glu Pro Phe Ser Leu Asp Pro Ser Lys Leu Asn Gly Ile Ser Pro  
 725 730 735

tct acg caa tcg att aga ttt ggg tct atg ttg ttg aat aga aca cgt 2256  
 Ser Thr Gln Ser Ile Arg Phe Gly Ser Met Leu Leu Asn Arg Thr Arg  
 740 745 750

aaa tag 2262  
 Lys

&lt;210&gt; 10

&lt;211&gt; 754

&lt;212&gt;

&lt;213&gt; Candida albicans

&lt;400&gt; 10

Met Ala Ala Ala Pro Pro Pro Pro Ala Lys Asn Gln Gly Lys Ala Lys			
1	5	10	15

Gln His Val Thr Gly Ala Arg Phe Arg Gln Arg Lys Ile Ser Val Lys			
20	25	30	

Gln Pro Leu Thr Ile Tyr Lys Gln Arg Asp Leu Pro Thr Leu Asp Ser			
35	40	45	

Asn Glu Leu Glu Pro Ser Gln Val His His Leu Asn Ser Asn Ala Ser			
50	55	60	

Ser Ser Ser Thr Gln Gln Pro Arg Asp Leu His Ala Val Glu Thr Gly			
65	70	75	80

Val Asp Lys Asn Glu Glu Glu Val His Leu Gln Gln Val Ile Asn			
85	90	95	

Ala Ala Gln Lys Ala Leu Leu Gly Ser Lys Lys Glu Glu Lys Ser Ser			
100	105	110	

Asp Met Tyr Ile Pro Thr Pro Asp Ala Ser Arg Ile Trp Pro Glu Ala			
115	120	125	

His Lys Tyr Tyr Lys Asp Gln Lys Phe Lys Gln Pro Glu Thr Tyr Ile			
130	135	140	

Lys Phe Ser Ala Thr Val Glu Asp Thr Val Gly Val Glu Tyr Asn Met			
145	150	155	160

Asp Glu Val Asp Glu Lys Phe Tyr Arg Glu Thr Leu Cys Lys Tyr Tyr  
165 170 175

Pro Lys Lys Lys Asn Lys Ser Asp Glu Asn Asn Arg Lys Cys Thr Glu  
180 185 190

Leu Glu Phe Glu Thr Ile Cys Asp Lys Leu Glu Lys Thr Ile Glu Ala  
195 200 205

Arg Gln Pro Phe Leu Ser Met Asp Pro Ser Asn Ile Leu Ser Tyr Glu  
210 215 220

Glu Leu Ser Ser Tyr Ile Val Asp Gln Phe Lys Ser Ala Val Lys Thr  
225 230 235 240

Ser Asn Pro Tyr Ile Val Thr Asn Gly Gly Asn Leu Glu Tyr Ile Ser  
245 250 255

Thr Thr Ala Leu Lys Glu Arg Leu Ser Lys Glu Ile Lys Tyr Glu Pro  
260 265 270

Phe Val Thr Ile Phe Asp Lys Asn Gln Met Ser Thr Ser Ala Val Arg  
275 280 285

Pro Ile Pro Lys Leu Phe Glu Leu Phe Gly Arg Pro Val Tyr Asp His  
290 295 300

Trp Lys Glu Arg Lys Ile Glu Arg Lys Gly Lys Thr Ile Gln Pro Thr  
305 310 315 320

Leu Lys Phe Glu Asp Pro Asn Ser Asn Glu Lys Glu Asn Asp Asn Asp  
325 330 335

Pro Tyr Ile Cys Phe Arg Arg Arg Glu Phe Arg Gln Ala Arg Lys Thr  
340 345 350

Arg Arg Ala Asp Thr Ile Gly Ala Glu Arg Ile Arg Ser Met Gln Lys  
355 360 365

Ser Leu His Arg Ala Arg Asp Leu Ile Met Ser Val Ser Glu Arg Glu  
370 375 380

Ile Leu Lys Leu Asp Asn Phe Gln Ala Glu His Glu Leu Phe Lys Ala  
385 390 395 400

Arg Cys Ala Thr Lys Ala Cys Lys Arg Glu Leu Asn Ile Lys Gly Asp  
405 410 415

Glu Tyr Leu Phe Phe Pro His Lys Lys Lys Ile Val Arg Thr Glu  
420 425 430

Asp Glu Glu Arg Glu Lys Lys Arg Glu Lys Lys Gln Asp Gln Glu  
435 440 445

Leu Ala Leu Lys Gln Gln Gln Ala Leu Gln Gln Gln Gln Gln Pro  
450 455 460

Pro Gln Pro Pro Gln Gln Ala Pro Ser Lys Gln Asp Gly Thr Ser Thr  
465 470 475 480

Ser Gln Pro Tyr Val Lys Leu Pro Pro Ala Lys Val Pro Asp Met Asp  
485 490 495

Leu Val Thr Val Ser Leu Val Leu Lys Glu Lys Asn Glu Thr Ile Lys  
500 505 510

Arg Ala Val Leu Glu Lys Leu Arg Lys Arg Lys Glu His Asp Lys Gly  
515 520 525

Phe Ile Asn Leu Thr Asp Asp Pro Tyr Gln Pro Phe Phe Asp Ile Ser  
530 535 540

Thr Asn Arg Ala Glu Glu Leu Ser His Ile Pro Tyr Ser Ser Ile Ala  
545 550 555 560

Ala Thr His Tyr His Gln Phe Asn Thr Ser Asn Tyr Met Asn Asp Gln  
565 570 575

Leu Lys Lys Leu Leu Glu Glu Lys Lys Pro Leu Pro Gly Val Lys Thr  
580 585 590

Phe Leu Gly Ser Asn Gly Glu Leu Val Pro Ser Lys Ala Phe Pro His  
595 600 605

Leu Ser Ser Leu Leu Glu Glu Lys Tyr Lys Ala Thr Ser Gly Tyr Ile  
610 615 620

Glu Arg Leu Leu Gln Ser Val Glu Thr Gln Asp Phe Ser Ser Tyr Thr  
625 630 635 640

Asn Gly Phe Lys Asp Val Glu Pro Lys Glu Thr Asn Glu Pro Val Met  
645 650 655

Ala Phe Pro Gln Arg Ile Arg Arg Val Gly Arg Ala Gly Arg Val  
660 665 670

Phe Leu Asp His Gln Gln Glu Tyr Pro Gln Pro Asn Phe Gln Gln Asp  
675 680 685

Thr Asp Arg Val Gly Gly Ile Pro Asp Val Tyr Cys Lys Glu Asp Ala  
690 695 700

Ile Lys Arg Leu Gln Ser Lys Trp Lys Phe Asp Thr Glu Tyr Lys Thr  
705 710 715 720

Thr Glu Pro Phe Ser Leu Asp Pro Ser Lys Leu Asn Gly Ile Ser Pro  
725 730 735

Ser Thr Gln Ser Ile Arg Phe Gly Ser Met Leu Leu Asn Arg Thr Arg  
740 745 750

Lys

<210> 11  
<211> 447  
<212> DNA  
<213> Candida albicans

<220>  
<221> CDS  
<222> (1) .. (447)

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1	5	10	15	
tat gaa tta gga ttt aaa gaa ggt caa ata caa gga aca aaa gat caa				96
Tyr Glu Leu Gly Phe Lys Glu Gly Gln Ile Gln Gly Thr Lys Asp Gln				
20	25	30		
tat tta gaa gga aaa gaa tat ggt tat caa act gga ttt caa cga ttt				144
Tyr Leu Glu Gly Lys Glu Tyr Gly Tyr Gln Thr Gly Phe Gln Arg Phe				
35	40	45		
tta atc att ggt tat att caa gaa tta atg aaa ttt tgg tta tcc cat				192
Leu Ile Ile Gly Tyr Ile Gln Glu Leu Met Lys Phe Trp Leu Ser His				
50	55	60		
ata gat caa tat aat aac tct tct tca ctt cgg aat cat ttg aat aat				240
Ile Asp Gln Tyr Asn Asn Ser Ser Leu Arg Asn His Leu Asn Asn				
65	70	75	80	
ttg gaa gat att atg gca caa att tct ata acg aat gga gat aaa gaa				288
Leu Glu Asp Ile Met Ala Gln Ile Ser Ile Thr Asn Gly Asp Lys Glu				
85	90	95		
gtt gaa gat tat gaa aaa aat att aaa aag gca aga aat aaa tta aga				336
Val Glu Asp Tyr Glu Lys Asn Ile Lys Lys Ala Arg Asn Lys Leu Arg				
100	105	110		

gtg ata gct agt ata act aaa gaa act tgg aaa att gat tca ttg gat 384  
 Val Ile Ala Ser Ile Thr Lys Glu Thr Trp Lys Ile Asp Ser Leu Asp  
 115 120 125

aat ttg gtg aaa gaa gta ggt gga act tta caa gtt agt gaa aac ccc 432  
 Asn Leu Val Lys Glu Val Gly Gly Thr Léu Gln Val Ser Glu Asn Pro  
 130 135 140

gat gat atg tgg tga 447  
 Asp Asp Met Trp  
 145

<210> 12  
<211> 149  
<212>  
<213> *Candida albicans*

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Tyr Glu Leu Gly Phe Lys Glu Gly Gln Ile Gln Gly Thr Lys Asp Gln  
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Tyr Leu Glu Gly Lys Glu Tyr Gly Tyr Gln Thr Gly Phe Gln Arg Phe  
 35 40 45

Leu Ile Ile Gly Tyr Ile Gln Glu Leu Met Lys Phe Trp Leu Ser His  
 50 55 60

Ile Asp Gln Tyr Asn Asn Ser Ser Leu Arg Asn His Leu Asn Asn  
 65 70 75 80

Leu Glu Asp Ile Met Ala Gln Ile Ser Ile Thr Asn Gly Asp Lys Glu  
 85 90 95

Val Glu Asp Tyr Glu Lys Asn Ile Lys Lys Ala Arg Asn Lys Leu Arg  
 100 105 110

Val Ile Ala Ser Ile Thr Lys Glu Thr Trp Lys Ile Asp Ser Leu Asp  
 115 120 125

Asn Leu Val Lys Glu Val Gly Gly Thr Leu Gln Val Ser Glu Asn Pro  
 130 135 140

Asp Asp Met Trp  
 145

<210> 13

<211> 966

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(966)

<400> 13

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 Met Gly Lys Arg Arg Val Asp Glu Glu Ser Asp Ser Asp Ile Asp Val  
 1 5 10 15

agt tca acc gat tca gaa act gaa tta gaa agc aca caa caa caa 96  
 Ser Ser Thr Asp Ser Glu Thr Glu Leu Glu Ser Thr Gln Gln Gln  
 20 25 30

caa caa caa gaa ggt gct act aca att caa gaa act gtt gat gtt gat 144  
 Gln Gln Gln Glu Gly Ala Thr Thr Ile Gln Glu Thr Val Asp Val Asp  
 35 40 45

ttt gat ttt ttt gat tta aat cct caa att gat ttg cat gct act aag 192  
 Phe Asp Phe Phe Asp Leu Asn Pro Gln Ile Asp Phe His Ala Thr Lys  
 50 55 60

aat ttt tta aga caa tta ttt ggt gat gat aat gga gaa ttt aat tta				240
Asn Phe Leu Arg Gln Leu Phe Gly Asp Asp Asn Gly Glu Phe Asn Leu				
65	70	75	80	
agt gaa ata gcc gat tta att tta cga gaa aat tcc gtg ggg aca tca				288
Ser Glu Ile Ala Asp Leu Ile Leu Arg Glu Asn Ser Val Gly Thr Ser				
85	90	95		
att aaa act gaa gga atg gaa agt gat cca ttt gca att tta agt gta				336
Ile Lys Thr Glu Gly Met Glu Ser Asp Pro Phe Ala Ile Leu Ser Val				
100	105	110		
att aat tta act aat aat tta aat gtg gcc gtg att aaa caa ttg att				384
Ile Asn Leu Thr Asn Asn Leu Asn Val Ala Val Ile Lys Gln Leu Ile				
115	120	125		
gaa tat att tca aat aaa acc aaa tct aaa act gaa ttc aat att att				432
Glu Tyr Ile Ser Asn Lys Thr Lys Ser Lys Thr Glu Phe Asn Ile Ile				
130	135	140		
ttg aaa aaa ttg tta acc aat cag aac gat act act aga gat agg aaa				480
Leu Lys Lys Leu Leu Thr Asn Gln Asn Asp Thr Thr Arg Asp Arg Lys				
145	150	155	160	
ttt aaa act gga tta ata att agt gaa aga ttt ata aat atg cca gtt				528
Phe Lys Thr Gly Leu Ile Ile Ser Glu Arg Phe Ile Asn Met Pro Val				
165	170	175		
gaa gtg att cca cca atg tat aaa atg ctt tta caa gaa atg gaa aaa				576
Glu Val Ile Pro Pro Met Tyr Lys Met Leu Leu Gln Glu Met Glu Lys				
180	185	190		
gct gaa gat gct cat gaa aat tat gaa ttt gat tat ttt tta att ata				624
Ala Glu Asp Ala His Glu Asn Tyr Glu Phe Asp Tyr Phe Leu Ile Ile				
195	200	205		

tca aga gtt tat caa tta gtt gat cca gtg gaa aga gaa gat gaa gat 672  
 Ser Arg Val Tyr Gln Leu Val Asp Pro Val Glu Arg Glu Asp Glu Asp  
 210 215 220

cac gaa aaa gaa tcc aat cgt aaa aag aag aac aag aat aag aag aag 720  
 His Glu Lys Glu Ser Asn Arg Lys Lys Asn Lys Asn Lys Lys Lys  
 225 230 235 240

aaa ttg gct aat aat gaa cca aaa cca ata gaa atg gat tat ttc cat 768  
 Lys Leu Ala Asn Asn Glu Pro Lys Pro Ile Glu Met Asp Tyr Phe His  
 245 250 255

ctt gaa gat caa att ttg gaa tca aat act caa ttt aaa gga ata ttt 816  
 Leu Glu Asp Gln Ile Leu Glu Ser Asn Thr Gln Phe Lys Gly Ile Phe  
 260 265 270

gaa tat aat aat gaa aat aaa caa gaa aca gat tca aga aga gta ttt 864  
 Glu Tyr Asn Asn Glu Asn Lys Gln Glu Thr Asp Ser Arg Arg Val Phe  
 275 280 285

act gaa tat ggt att gat cct aaa tta agt tta atc tta att gat aaa 912  
 Thr Glu Tyr Gly Ile Asp Pro Lys Leu Ser Leu Ile Leu Ile Asp Lys  
 290 295 300

gat aat tta gct aaa tca gtc att gaa atg gaa caa caa ttc cca cct 960  
 Asp Asn Leu Ala Lys Ser Val Ile Glu Met Glu Gln Gln Phe Pro Pro  
 305 310 315 320

cca taa 966  
 Pro

<210> 14

<211> 322

<212>

<213> Candida albicans

&lt;400&gt; 14

Met Gly Lys Arg Arg Val Asp Glu Glu Ser Asp Ser Asp Ile Asp Val  
1 5 10 15

Ser Ser Thr Asp Ser Glu Thr Glu Leu Glu Ser Thr Gln Gln Gln  
20 25 30

Gln Gln Gln Glu Gly Ala Thr Thr Ile Gln Glu Thr Val Asp Val Asp  
35 40 45

Phe Asp Phe Phe Asp Leu Asn Pro Gln Ile Asp Phe His Ala Thr Lys  
50 55 60

Asn Phe Leu Arg Gln Leu Phe Gly Asp Asp Asn Gly Glu Phe Asn Leu  
65 70 75 80

Ser Glu Ile Ala Asp Leu Ile Leu Arg Glu Asn Ser Val Gly Thr Ser  
85 90 95

Ile Lys Thr Glu Gly Met Glu Ser Asp Pro Phe Ala Ile Leu Ser Val  
100 105 110

Ile Asn Leu Thr Asn Asn Leu Asn Val Ala Val Ile Lys Gln Leu Ile  
115 120 125

Glu Tyr Ile Ser Asn Lys Thr Lys Ser Lys Thr Glu Phe Asn Ile Ile  
130 135 140

Leu Lys Lys Leu Leu Thr Asn Gln Asn Asp Thr Thr Arg Asp Arg Lys  
145 150 155 160

Phe Lys Thr Gly Leu Ile Ile Ser Glu Arg Phe Ile Asn Met Pro Val  
165 170 175

Glu Val Ile Pro Pro Met Tyr Lys Met Leu Leu Gln Glu Met Glu Lys  
180 185 190

Ala Glu Asp Ala His Glu Asn Tyr Glu Phe Asp Tyr Phe Leu Ile Ile  
 195 200 205

Ser Arg Val Tyr Gln Leu Val Asp Pro Val Glu Arg Glu Asp Glu Asp  
 210 215 220

His Glu Lys Glu Ser Asn Arg Lys Lys Lys Asn Lys Lys Lys Lys Lys  
 225 230 235 240

Lys Leu Ala Asn Asn Glu Pro Lys Pro Ile Glu Met Asp Tyr Phe His  
 245 250 255

Leu Glu Asp Gln Ile Leu Glu Ser Asn Thr Gln Phe Lys Gly Ile Phe  
 260 265 270

Glu Tyr Asn Asn Glu Asn Lys Gln Glu Thr Asp Ser Arg Arg Val Phe  
 275 280 285

Thr Glu Tyr Gly Ile Asp Pro Lys Leu Ser Leu Ile Leu Ile Asp Lys  
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Asp Asn Leu Ala Lys Ser Val Ile Glu Met Glu Gln Gln Phe Pro Pro  
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Pro

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 attgagggag cacttgataa tagtgattt aatgcggatg ttacagcaca cacggcttgtt 240  
 acagatgcaa atccattaag aacagtattt ttgatcaagt ttgacgatcc tgtttttaattt 300  
 agagagagtt tgagattttgg 320

&lt;210&gt; 16

&lt;211&gt; 295

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 16

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 ttatattgtcc aaagaggaaa gagattatac acacaaatat ttccagattt tgactcaattt 180  
 atataacaac tgtttccca aaaaactacc acaaatgttg acctattttgg atgacaccag 240  
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&lt;210&gt; 17

&lt;211&gt; 392

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 17

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 gcaccaaaag atagttcatc cgacatacgt actcatatgg gactccatca tcattggag 120  
 accccacata tggcagggtt tacattgggt gagttggccc atttagccag atcgactttt 180

gctggacaaa gatgcttgag cattcaaaca tttagggagaa ttttccataa attgggatta 240  
 cataaataca gtataactacc aaaccagctc aatgatcaga tttttacaga tgaatcaaaa 300  
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 tataattta aatgtggccg tgattaaaca attgattgaa tatattttaa ataaaaccaa 240  
 atctaaaact gaattcaata ttatggaa aaaattgtta accaatcaga acgatactac 300  
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